



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/517,333
Source: PCT
Date Processed by STIC: 12-22-04

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 05/17/04



PCT

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/517,333

DATE: 12/22/2004
 TIME: 08:53:36

Input Set : A:\ISPT1011.ST25.txt
 Output Set: N:\CRF4\12222004\J517333.raw

3 <110> APPLICANT: Baker, Brenda F.
 4 Freier, Susan M.
 5 Dobie, Kenneth W.
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1
 8 EXPRESSION
 10 <130> FILE REFERENCE: ISPT-1011
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/517,333
 C--> 12 <141> CURRENT FILING DATE: 2004-12-09
 12 <150> PRIOR APPLICATION NUMBER: PCT/US03/18003
 13 <151> PRIOR FILING DATE: 2003-06-09
 15 <150> PRIOR APPLICATION NUMBER: US 10/167,034
 16 <151> PRIOR FILING DATE: 2002-06-10
 18 <160> NUMBER OF SEQ ID NOS: 143
 20 <170> SOFTWARE: PatentIn version 3.3
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 23 <211> LENGTH: 20
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Antisense Oligonucleotide
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 31 tccgtcatcg ctcctcaggg 20
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 35 <211> LENGTH: 20
 36 <212> TYPE: DNA
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 47 <211> LENGTH: 20
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Antisense Oligonucleotide
 54 <400> SEQUENCE: 3
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 59 <211> LENGTH: 3590
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Homo sapiens
 64 <220> FEATURE:

(pg. 6-8) ✓

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Output Set: N:\CRF4\12222004\J517333.raw

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73 1 5 10		
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76 Ala Pro Gly Ala Gln His Phe Leu Tyr Glu Val Pro Pro Trp Val Met		
77 15 20 25		
79 tgc cgc ttc tac aaa gtg atg gac gcc ctg gag ccc gcc gac tgg tgc	208	
80 Cys Arg Phe Tyr Lys Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys		
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84 Gln Phe Ala Ala Leu Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys		
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87 gag cgc tcc ggg cag cgc acg gcc agc gtc ctg tgg ccc tgg atc aac	304	
88 Glu Arg Ser Gly Gln Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn		
89 60 65 70 75		
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92 Arg Asn Ala Arg Val Ala Asp Leu Val His Ile Leu Thr His Leu Gln		
93 80 85 90		
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97 95 100 105		
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109 140 145 150 155		
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113 160 165 170		
115 cca tct cca gcc cct tct acc aag cca ggc cca gag agc tca gtg	640	
116 Pro Ser Pro Ala Pro Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val		
117 175 180 185		
119 tcc ctc ctg cag gga gcc cgc ccc tct ccg ttt tgc tgg ccc ctc tgt	688	
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121 190 195 200		
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124 Glu Ile Ser Arg Gly Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly		
125 205 210 215		
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128 Glu Gly Phe Gly Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val		
129 220 225 230 235		

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Input Set : A:\ISPT1011.ST25.txt
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132	Tyr	Ala	Val	Lys	Arg	Leu	Lys	Glu	Asn	Ala	Asp	Leu	Glu	Trp	Thr	Ala	
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135	gtg	aag	cag	agc	ttc	ctg	acc	gag	gtg	gag	cag	ctg	tcc	agg	ttt	cgt	880
136	Val	Lys	Gln	Ser	Phe	Leu	Thr	Glu	Val	Glu	Gln	Leu	Ser	Arg	Phe	Arg	
137				255				260							265		
139	cac	cca	aac	att	gtg	gac	ttt	gct	ggc	tac	tgt	gct	cag	aac	ggc	ttc	928
140	His	Pro	Asn	Ile	Val	Asp	Phe	Ala	Gly	Tyr	Cys	Ala	Gln	Asn	Gly	Phe	
141				270				275							280		
143	tac	tgc	ctg	gtg	tac	ggc	ttc	ctg	ccc	aat	ggc	tcc	ctg	gag	gac	cgt	976
144	Tyr	Cys	Leu	Val	Tyr	Gly	Phe	Leu	Pro	Asn	Gly	Ser	Leu	Glu	Asp	Arg	
145				285				290							295		
147	ctc	cac	tgc	cag	acc	cag	gcc	tgc	cca	cct	ctc	tcc	tgg	cct	cag	cga	1024
148	Leu	His	Cys	Gln	Thr	Gln	Ala	Cys	Pro	Pro	Leu	Ser	Trp	Pro	Gln	Arg	
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151	ctg	gac	atc	ctt	ctg	ggt	aca	gcc	cg	gca	att	cag	ttt	cta	cat	cag	1072
152	Leu	Asp	Ile	Leu	Leu	Gly	Thr	Ala	Arg	Ala	Ile	Gln	Phe	Leu	His	Gln	
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155	gac	agc	ccc	agc	ctc	atc	cat	gga	gac	atc	aag	agt	tcc	aac	gtc	ctt	1120
156	Asp	Ser	Pro	Ser	Leu	Ile	His	Gly	Asp	Ile	Lys	Ser	Ser	Asn	Val	Leu	
157				335				340							345		
159	ctg	gat	gag	agg	ctg	aca	ccc	aag	ctg	gga	gac	ttt	ggc	ctg	gcc	cg	1168
160	Leu	Asp	Glu	Arg	Leu	Thr	Pro	Lys	Leu	Gly	Asp	Phe	Gly	Leu	Ala	Arg	
161				350				355							360		
163	tcc	agc	cgc	ttt	gcc	ggg	tcc	agc	ccc	agc	cag	agc	agc	atg	gtg	gcc	1216
164	Phe	Ser	Arg	Phe	Ala	Gly	Ser	Ser	Pro	Ser	Gln	Ser	Ser	Met	Val	Ala	
165				365				370							375		
167	cgg	aca	cag	aca	gtg	cgg	ggc	acc	ctg	gcc	tac	ctg	ccc	gag	gag	tac	1264
168	Arg	Thr	Gln	Thr	Val	Arg	Gly	Thr	Leu	Ala	Tyr	Leu	Pro	Glu	Glu	Tyr	
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171	atc	aag	acg	gga	agg	ctg	gct	gtg	gac	acg	acc	ttc	agc	ttt	ggg	1312	
172	Ile	Lys	Thr	Gly	Arg	Leu	Ala	Val	Asp	Thr	Asp	Thr	Phe	Ser	Phe	Gly	
173				400				405							410		
175	gtg	gta	gtg	cta	gag	acc	ttt	gg	gct	cag	agg	gct	gtg	aag	acg	cac	1360
176	Val	Val	Val	Leu	Glu	Thr	Leu	Ala	Gly	Gln	Arg	Ala	Val	Lys	Thr	His	
177				415				420							425		
179	gg	gcc	agg	acc	aag	tat	ctg	aaa	gac	ctg	gtg	gaa	gag	gag	gct	gag	1408
180	Gly	Ala	Arg	Thr	Lys	Tyr	Leu	Lys	Asp	Leu	Val	Glu	Glu	Ala	Glu		
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183	gag	gct	gga	gtg	gct	ttt	aga	agc	acc	cag	agc	aca	ctg	caa	gca	gg	1456
184	Glu	Ala	Gly	Val	Ala	Leu	Arg	Ser	Thr	Gln	Ser	Thr	Leu	Gln	Ala	Gly	
185				445				450							455		
187	ctg	gct	gca	gat	gcc	tgg	gct	ccc	atc	gcc	atg	cag	atc	tac	aag		1504
188	Leu	Ala	Ala	Asp	Ala	Trp	Ala	Ala	Pro	Ile	Ala	Met	Gln	Ile	Tyr	Lys	
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196	Gly	Leu	Gly	Gln	Leu	Ala	Cys	Cys	Cys	Leu	His	Arg	Arg	Ala	Lys	Arg
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201		510				515					520					
203	gtg	gtg	gcg	ggg	gtg	ccc	ggg	cat	ttg	gag	gcc	gcc	agc	tgc	atc	ccc
204	Val	Val	Ala	Gly	Val	Pro	Gly	His	Leu	Glu	Ala	Ala	Ser	Cys	Ile	Pro
205		525				530					535					
207	cct	tcc	ccg	cag	gag	aac	tcc	tac	gtg	tcc	agc	act	ggc	aga	gcc	cac
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212	Ser	Gly	Ala	Ala	Pro	Trp	Gln	Pro	Leu	Ala	Ala	Pro	Ser	Gly	Ala	Ser
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216	Ala	Gln	Ala	Ala	Glu	Gln	Leu	Gln	Arg	Gly	Pro	Asn	Gln	Pro	Val	Glu
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224	Leu	Thr	Pro	Ser	Cys	Pro	Leu	Asp	Pro	Ala	Pro	Leu	Arg	Glu	Ala	Gly
225	605		610			615					620		625		630	635
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237		655			660						665		670		675	680
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253	tcatggtgca	cgagtcttca	gcactctgcc	ggcagtggggg	gtggggggcc	atgccccggg										2338
255	ggggagagaag	gagggtggccc	tgctgttcta	ggctctgtgg	gcataggccag	gcagagtgga										2398
257	accctgcctc	catgccagca	tctgggggca	aggaaggctg	gcatcatcca	gtgaggaggc										2458
259	tggcgcatgt	tgggaggctg	ctggctgcac	agaccctgtga	ggggaggaga	ggggctgtcg										2518
261	tgcaggggtg	tggagtaggg	agctggctcc	cctgagagcc	atgcaggcg	tctgcagccc										2578
263	aggcctctgg	cagcagctct	ttgcccatact	ctttggacag	tggccaccc	gcacaatggg										2638
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271	taaaactatta	gcctggcgtg	gtagcgcacg	cctgtggtcc	cagctgtgg	ggaggctgaa	2878									
273	gtaggaggat	catttatgct	tgggaggtcg	aggctgcagt	gagtcatgat	tgtatgactg	2938									
275	cactccagcc	tgggtgacag	agcaagaccc	tgttcaaaa	agaaaaaccc	tggaaaaagt	2998									
277	gaagtatggc	tgtaaatctc	atggttcaat	cctagcaaga	agcgagaatt	ctgagatcct	3058									
279	ccagaaaatgc	gagcagcacc	cacctccaaac	ctcgggcccag	tgttccagg	cttactggg	3118									
281	gacctgcgag	ctggccta	atgtggcct	gcaagccagg	ccatccctgg	gcgccacaga	3178									
283	cgagctccga	gccaggtcag	gttcggagg	ccacaagctc	agectcaggc	ccaggcactg	3238									
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287	agtgagaagc	ccctgaaagg	cagaaaagg	gggagcatgg	cagacaggg	aggaaacat	3358									
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291	gtgtcctctt	gcgtgtccaa	aagtggccca	gggctgttagc	acaggctca	cagtgatttt	3478									
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310					20			25					30			
313	Val	Met	Asp	Ala	Leu	Glu	Pro	Ala	Asp	Trp	Cys	Gln	Phe	Ala	Ala	Leu
314					35			40					45			
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318					50			55					60			
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322					65			70			75		80			
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326						85			90				95			
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330						100			105				110			
333	Thr	Thr	Ala	Pro	Arg	Pro	Ser	Ser	Ile	Pro	Ala	Pro	Ala	Glu	Ala	Glu
334						115			120				125			
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342						145			150			155		160		
345	Val	Pro	Ser	Pro	Ala	Ser	Leu	Trp	Pro	Pro	Pro	Pro	Ser	Pro	Ala	Pro
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349	Ser	Ser	Thr	Lys	Pro	Gly	Pro	Glu	Ser	Ser	Val	Ser	Leu	Leu	Gln	Gly
350							180			185			190			
353	Ala	Arg	Pro	Ser	Pro	Phe	Cys	Trp	Pro	Leu	Cys	Glu	Ile	Ser	Arg	Gly
354							195			200			205			
357	Thr	His	Asn	Phe	Ser	Glu	Glu	Leu	Lys	Ile	Gly	Glu	Gly	Gly	Phe	Gly
358							210			215			220			
361	Cys	Val	Tyr	Arg	Ala	Val	Met	Arg	Asn	Thr	Val	Tyr	Ala	Val	Lys	Arg

10/5/7, 333

Page 6

<210> 29
<211> 20
<212> DNA
<213> Artificial
<220>
<223>
<400> 29
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P15 explain

Artificial

PTS
InStat

The types of errors shown exist throughout
the sequence listing. Please check subsection
sequences for similar errors.

mandatory

if <213>

response is Artificial

Unknown, pls explain
in section <220>-<223>

See pg. 7 for
error explanation

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 625

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,6,7,8,9,10,11,16,17,18,19,20,21,22,23,24,25,26,27,28,31,32,33,34,35

Seq#:36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59

Seq#:60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,80,81,82,83,84

Seq#:85,86

Use of <220> Feature(NEW RULES):

Error Explanation: 2

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:29,79

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/517,333

DATE: 12/22/2004

TIME: 08:53:37

Input Set : A:\ISPT1011.ST25.txt

Output Set: N:\CRF4\12222004\J517333.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:600

L:1235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29

L:1237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial SequenceL:1237 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence

L:1237 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:1237

L:1832 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:79

L:1834 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:79, <213>
ORGANISM:Artificial Sequence

L:1834 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:79, <213>

ORGANISM:Artificial Sequence

L:1834 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:79,Line#:1834